## IN THE SPECIFICATION:

Please replace Paragraph No. 00055 with the following paragraph:

The present invention provides purified and isolated polynucleotides (*e.g.*, DNA sequences and RNA transcripts, both sense and complementary antisense strands, both single- and double-stranded, including splice variants thereof) that encode unknown G protein-coupled receptors heretofore termed novel GPCRs, or nGPCRs. The gene described herein is referred to as nGPCR-2644. Table 1 below identifies the SEQ ID NO: of the gene sequence, the SEQ ID NO: of the polypeptide encoded thereby, and the U.S. Provisional Application in which the gene sequence has been disclosed.

Table 1

nGPCR	Nucleotide Sequence (SEQ ID NO:)	Amino acid Sequence (SEQ ID NO:)	Originally filed in:
2644	1	2	A

## Legend

A = Ser. No. 60/199,558

Please replace Paragraph No. 00119 with the following paragraph:

Variant polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Amino acids can be classified according to physical properties and contribution to secondary and tertiary protein structure. A conservative substitution is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are set out in Table 2 (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96), immediately below.

Table 2

Conservative Substitutions I

SIDE CHAIN

<b>CHARACTERISTIC</b>	<b>AMINO ACID</b>
Aliphatic	
Non-polar	GAP
	LLV
Polar - uncharged	CSTM
	N Q
Polar - charged	D E
	KR
Aromatic	HFWY
Other	NQDE

Please replace Paragraph No. 00120 with the following paragraph:

Alternatively, conservative amino acids can be grouped as described in Lehninger, (Biochemistry, Second Edition; Worth Publishers, Inc. NY, NY (1975), pp.71-77) as set out in Table 3, below.

Table 3
Conservative Substitutions II

## SIDE CHAIN **CHARACTERISTIC** AMINO ACID Non-polar (hydrophobic) A. Aliphatic: ALIVP F W B. Aromatic: C. Sulfur-containing: М D. Borderline: G Uncharged-polar A. Hydroxyl: STYΝQ B. Amides: C. Sulfhydryl: C

Please replace Paragraph No. 00236 with the following paragraph:

Positively Charged (Basic):

Negatively Charged (Acidic):

D. Borderline:

G

KRH

DΕ

-- The following Table 5 contains the sequences of the polynucleotides and polypeptides of the invention. The transmembrane domains within the polypeptide sequence are identified by underlining, and start and stop sites are identified by bold text.

## Table 5

The following DNA sequence nGPCR-2644 <SEQ ID NO. 1> was identified in *H. sapiens*:

CONTROL FIGURE TO THE OFFICE OF A GRADIES AND A GRADIES OF A GRADIES O ACCCACCGGTGCCGGCACTGAGCCTGCAACCTGTCTCACGCCCTCTGECTGTTGCCATGA CCAAAATGCCAATCAGCCTGGCCCAGGCATCATCCGCTCAACCGTGCTGGTTATCTTCC TO TIGO AGGIGA COA A COGITITIATO TITA A COTO CITO DI CACOGA ODIGO TO CACATITI ment nergodor otsak<mark>raataaada</mark>ndtotatadottotatiologiaadant (AA/A/F) ACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTCGCCTTCGCCAGCGTCAACACCA TT STONT AGTGTGAGTGAATOG TA DITGTGCATCATC CACCO ICTO ICCTAM MCUTMCA AGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACCTGGATTGTGGCCATCCTGC A KARCA TOCTOTACTOTACGEOTG EGGCCAGSCTSCCPTTGATGAG DGCAATSCTCTCT GCTCCATGATCTGGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTTCCTTCATCG TIMITTI MACTEMITGINATEA PIECO POCTACIO O SIGITIFICAÇÃO COGRA ASC ACCATOCTCTGCTGTACAATGT DAA SAGACACAGCTTG SAAGTGCGAG POAAGGACTCTG tio la bant er gortigar baggeagcagagaagaagaegae en tid cae eatoagat. Mai ya TCCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCTCCTCCCCCAGGT GOTA COASTIGOAAS OT GOTAAAST SATOT TOATOATOAT IT I DTOD IA ISTROTAT DOO MOA STOGGTGATCACCATAAT JAT DIGGCTTTTCTTCGTGCAGTGCI GCATCCACCCCT ATGTCTATGGCTACATGCACAA SACCATTAAGAAGGAAA POCAGGACATGCTGAAGAAGT TO TITITO NAROSARAS NOCOCIGAAAGAAGATAGOCACOCAGACOTGOCOG HAACAHA HG GTOGGACTGAAGGCAAGATIGT DOOTTCCTACGATTCT BOTADITTT DOT**TGA**AGTTAGT TOTAR GODARACOTT GRACTET ICA FARCACEGAGARACAR SA ESAGATT FOTTITORATE CTOTTOACORCAAGGTAGATAAATATATAGAAGAGGCAGGAACTEGGETOTOT OOTAAA AGCATGGACTTGAGGATTCT JACTGAAATT

The following amino acid sequence <SEQ ID NO. 2> is a predicted amino acid sequence derived from the DNA sequence of SEQ ID NO. 1:

<SEO ID NO. 2 ·

MTGTGTNSTRESNOSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKFQ
LLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTI
VVVSVDRYLGIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFTERNALGS
MIWHASFSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVEVKDCVEN
EDEESAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY
CFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKE
KFIKEDSHFDLPGTEGGTEGKIVPSYDSATFF

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